

## Appendix A

Clustal V alignment of the amino acid sequences having SEQ ID NOS:2, 4, and 6 in the instant application with the cobalamin independent methionine synthases from *E. coli* (NCBI gi No. 836660), *Catharanthus roseus* (NCBI gi No. 1362086), *Coleus blumei* (amino acids 21-84, NCBI gi No. 974782), *Arabidopsis thaliana* (NCBI gi No. 2738248), *Mesembryanthemum crystallinum* (NCBI gi No. 1814403), *Arabidopsis thaliana* (NCBI gi No ), and *Solanum tuberosum* (NCBI gi No. 8339545). Amino acids conserved among all the sequences are indicated by an asterisk (\*) below the alignment and those conserved only among the plant sequences are indicated by a plus sign (+). The conserved domain containing the active site cysteine (corresponding to *E. coli* 726) is shown boxed.

	1	60
836660	MTILNHTLGFPRVGLRRELKKAQESYWAGNSTREELLAVGRELRARHWDQQKQAGIDLLP	
1362086	MA--SHIVGYPRMGPKRELKFALESFWDKKSSAEDLQKVAADLRSSIWKQMADAGIKYIP	
SEQIDNO02	MA--SHIVGYPRMGPKRELKFALESFWDGKSSAEDLEKVATDLRSSIWKQMSEAGIKYIP	
SEQIDNO04	MA--SHIVGYPRMGPKRELKFALESFWDGKSSAEDLQKVAADLRSSIWKQMAGAGIKYIP	
SEQIDNO6	MA--SHIVGYPRMGPKRELKFALESFWDGKSSAEDLKKVAADLRSSIWKQMADAGIKYIP	
8439545	MA--SHVVGYPRMGPKRELKFALESFWDGKSSAEDLKKVSADLRSSIWKQMSDAGIKYIP	
CAA89019	MA--SHIVGYPRMGPKRELKFALESFWDGKSSAEDLEKCQLILGIHL-KQMSDAGIKYIP	
AAB41896	MA--SHIVGYPRMGPKRELKFALESFWDGKSTAEDLKKVSADLRSSIWKQMADAGIKYIP	
2738248	MA--SHIVGYPRMGPKRELKFALESFWDGKSTAEDLQKVSADLRSSIWKQMSAAGTKFIP	
	*+ * +* +**+*++*****+*+***+++ ++ +*+* + * *+* +*+** +** + * +*	
	61	
836660	VGDFAWYDHVLTTSLLLGNVPARHQNKDGSDIDTLFRIGRGRAPTGEPAAAAEMTKWFN	120
1362086	SNTFSYYDQVLDTATMLGAVPPRYNFAGGEIGFDTYFSMARGNASV----PAMEMTKWFD	
SEQIDNO02	SNTSSYYDQVLDTTAMLGAVPERYSWTGGEIGLSTYFSMARGNATV----PAMEMTKWFD	
SEQIDNO04	SNTFSFYDQLLDATATLGAVPPRYGWTGGEIGFDTYFSMARGNATV----PAMEMTKWFD	
SEQIDNO6	SNTFSYYDQVLDTTAMLGAVPARYNWAGGEIAFDTYFSMARGNASV----PAMEMTKWFD	
8439545	SNTFSYYDQVLDTTAMLGAVPSRYNWTGGEIEFGTYFSMARGNASV----PAMEMTKWFD	
CAA89019	SNTFSYYDQVLDTTAMLGAVPPRYNWTGGEIGFSTYFSMARGNASV----PAMEMTKWFD	
AAB41896	SNTFSYYDQVLDTTAMLGAVPPRYGWTGGEIEFDVYFSMARGNASV----PAMEMTKWFD	
2738248	SNTFAHYDQVLDTTAMLGAVPPRGYTGGEIGLDVYFSMARGNASV----PAMEMTKWFD	
	+++ *** *+ ***+* *+ +*++ +*++*+*+* + +*+*****+	
	121	
836660	TNYHYMVPEFKGQQFKLTWTQLLDEVDEALALGHKVKPVLLGPVTWLWLKG-VKGEQ--	180
1362086	TNYHYIVPELGPEVNFSYASHKAVNEYKEAKELGVDTVPVLVGPVTFLLLSKPAKGVEKT	
SEQIDNO02	TNYHFIVPELGPSTKFTYASHKAVSEYKEAKALGIDTVPLVGPVSYLLLSKPAKGVEKS	
SEQIDNO04	TNYHFIVPELGPDVNFTXASQKAVDEYKEAKALGVDTIPVLVGPVTYLLLSKPAKGVEKS	
SEQIDNO6	TNYHFIVPELGPDVNFSYASHKAVDEYKEAKGLGVDTVPVLIGPVSYLLLSKPAKGVEKS	
8439545	TNYHFIVPELGPDVNFSYASHKAVNEYKEAKAQGVDTVPVLVGPVSYLLLSKPAKGVEKS	
CAA89019	TNYHFIVPELGPDKFSYASHKAVNEYKEAKALGVDTVPVLVGPVSYLLLSKPAKGVEKT	
AAB41896	TNYHFIVPELGPDVNFSYASHKAVLEYKEAKALGVDTVPVLVGPVSYLLLSQAKGVDKS	
2738248	TNYHYIVPELGPEVNFSYASHKAVNEYKEAKALGVDTVPVLVGPVSYLLLSKAAGGVDKS	
	***** +**** ++ * ++ +++ *++*+ * ++ *** *** *+*** +*** +	



421 480  
 VYEVRAEAQRARFKLPAWPTTIGSFQQTTEIRTLRLDFKKGNLDANNYRTGIAEHIKQA  
 TVSARLDAQQKKLNLPVLPTTIGSFQQTLELRRVRREYKAKKISEDDYVKAIKEEISKV  
 TVSARLDAQQKKLNLPVLPTTIGSFQQTVELRRVRREYKAKKITEDEYISAIKEEISKV  
 NVSARLDAQQKKLNLPILPTTIGSFQQTVELRRVRREFKANKISEEEYVKSIKEEIRKV  
 NVSSRLDAQQKKLNLPVLPTTIGSFQQTVELRRVRREYKAKKISEEEYVKAIAEIKKV  
 NVSARLDAQQKKLNLPILPTTIGSFQQTVELRRVRREYKAKKISEEEYVKAITEEIKKV  
 NVSARLDAQQKKLNLPILPTTIGSFQQTVELRRVRREFKPTRISEEEYVKAIKEEINKV  
 TVSSRLDAQQKKLNLPILPTTIGSFQQTVELRRVRREYKAKKISEEEYVKAIKEEISKV  
 NVSARLDAQQKKLNLPILPTTIGSFQQTVELRRVRREYKAKKVSSEEDYVKAIKEEIKKV  
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661

720

721

771